



SEQUENCE LISTING

<110> Protein Design Labs

<120> ANTIBODIES AGAINST GPR64 AND USES THEREOF

<130> 05882.0177.NPUS01

<160> 30

<170> PatentIn version 3.2

<210> 1

<211> 4665

<212> DNA

<213> Homo sapiens

<400> 1

```
agccagcccg aggacgcgag cggcaggtgt gcacagaggt tctccacttt gttttctgaa      60
ctcgcggtca ggatggtttt ctctgtcagg cagtgtggcc atgttggcag aactgaagaa      120
gttttactga cgttcaagat attccttgtc atcatttgtc ttcattgtcg tcttggaaca      180
tccctggaag aagatactga taattccagt ttgtcaccac cacctgctaa attatctgtt      240
gtcagttttg cccctctctc caatgaggtt gaaacaacaa gcctcaatga tgttacttta      300
agcttactcc cttcaaacga aacagaaaaa actaaaatca ctatagtaaa aaccttcaat      360
gcttcaggcg tcaaacccca gagaaatatc tgcaatttgt catctatttg caatgactca      420
gcatttttta gaggtgagat catgtttcaa tatgataaag aaagcactgt tccccagaat      480
caacatataa cgaatggcac cttaactgga gtcctgtctc taagtgaatt aaaacgctca      540
gagctcaaca aaaccctgca aaccctaagt gagacttact ttataatgtg tgctacagca      600
gaggcccaaa gcacattaaa ttgtacattc acaataaaac tgaataatac aatgaatgca      660
tgtgtgcaa tagccgcttt ggaaagagta aagattcgac caatggaaca ctgctgctgt      720
tctgtcagga taccctgccc ttcttcccca gaagagttgg gaaagcttca gtgtgacctg      780
caggatccca ttgtctgtct tgctgaccat ccacgtggcc caccattttc ttccagccaa      840
tccatcccag tgggtgcctcg ggccactgtg ctttcccagg tccccaaagc tacctctttt      900
gctgagcctc cagattattc acctgtgacc cacaatgttc cctctccaat aggggagatt      960
caaccctttt caccctcagcc tttagctccc atagcttcca gccctgccat tgacatgccc     1020
ccacagtctg aaacgatctc ttcccctatg ccccaaacc atgtctccgg caccctacct     1080
cctgtgaaag cctcattttc ctctcccacc gtgtctgccc ctgcgaatgt caacactacc     1140
agcgcacctc ctgtccagac agacatcgtc aacaccagca gtatttctga tcttgagaac     1200
caagtgttgc agatggagaa ggctctgtcc ttgggcagcc tggagcctaa cctcgcagga     1260
gaaatgatca accaagtcag cagactcctt cattccccgc ctgacatgct ggccctctg     1320
gctcaaagat tgctgaaagt agtggatgac attggcctac agctgaactt ttcaaacacg     1380
```

actataagtc	taacctcccc	ttcttttggt	ctggctgtga	tcagagtga	tgccagtagt	1440
ttcaacacaa	ctacctttgt	ggcccaagac	cctgcaaadc	ttcaggtttc	tctggaaacc	1500
caagctcctg	agaacagtat	tggcacaatt	actcttcctt	catcgctgat	gaataattta	1560
ccagctcatg	acatggagct	agcttccagg	gttcagttca	atTTTTTTga	aacacctgct	1620
ttgtttcagg	atccttccct	ggagaacctc	tctctgatca	gctacgtcat	atcatcgagt	1680
gttgcaaacc	tgaccgtcag	gaacttgaca	agaaacgtga	cagtcacatt	aaagcacatc	1740
aacccgagcc	aggatgagtt	aacagtgaga	tgtgtatttt	gggacttggg	cagaaatggt	1800
ggcagaggag	gctggtcaga	caatggctgc	tctgtcaaag	acaggagatt	gaatgaaacc	1860
atctgtacct	gtagccatct	aacaagcttc	ggcgttctgc	tggacctatc	taggacatct	1920
gtgctgcctg	ctcaaatgat	ggctctgacg	ttcattacat	atattggttg	tgggctttca	1980
tcaatttttc	tgtcagtgac	tcttgtaacc	tacatagctt	ttgaaaagat	ccggagggat	2040
tacccttcca	aaatcctcat	ccagctgtgt	gctgctctgc	ttctgctgaa	cctggctcttc	2100
ctcctggact	cgtggattgc	tctgtataag	atgcaaggcc	tctgcatctc	agtggctgta	2160
tttcttcatt	atTTTctctt	ggctctcattc	acatggatgg	gcctagaagc	attccatatg	2220
tacctggccc	ttgtcaaagt	atttaatact	tacatccgaa	aatacatcct	taaattctgc	2280
attgtcgggt	gggggggtacc	agctgtgggt	gtgaccatca	tcctgactat	atccccagat	2340
aactatgggc	ttggatccta	tgggaaattc	cccaatgggt	caccggatga	cttctgctgg	2400
atcaacaaca	atgcagtatt	ctacattacg	gtgggtgggag	atttctgtgt	gatatttttg	2460
ctgaacgtca	gcatgttcat	tgtgggtcctg	gttcagctct	gtcgaattaa	aaagaagaag	2520
caactgggag	cccagcgaaa	aaccagtatt	caagacctca	ggagtatcgc	tggccttaca	2580
tttttactgg	gaataacttg	gggctttgcc	ttctttgcct	ggggaccagt	taacgtgacc	2640
ttcatgtatc	tgtttgccat	ctttaataacc	ttacaaggat	ttttcatatt	catctttttac	2700
tgtgtggcca	aagaaaatgt	caggaagcaa	tggaggcggt	atctttgttg	tggaaagtta	2760
cggctggctg	aaaattctga	ctggagtaaa	actgctacta	atggttttaa	gaagcagact	2820
gtaaaccaag	gagtgtccag	ctcttcaaat	tccttacagt	caagcagtaa	ctccactaac	2880
tccaccacac	tgctagtga	taatgattgc	tcagtacacg	caagcgggaa	tggaaatgct	2940
tctacagaga	ggaatggggg	ctcttttagt	gttcagaatg	gagatgtgtg	ccttcacgat	3000
ttcactggaa	aacagcacat	gtttaacgag	aaggaagatt	cctgcaatgg	gaaaggccgt	3060
atggctctca	gaaggacttc	aaagcgggga	agcttacact	ttattgagca	aatgtgattc	3120
ctttcttcta	aaatcaaagc	atgatgcttg	acagtgtgaa	atgtccaatt	ttacctttta	3180
cacaatgtga	gatgtatgaa	aatcaactca	ttttattctc	ggcaacatct	ggagaagcat	3240
aagctaatta	agggcgatga	ttattattac	aagaagaaac	caagacatta	caccatgggt	3300

tttagacatt tctgatttgg tttcttatct ttcattttat aagaaggttg gttttaaaca	3360
atacactaag aatgactcct ataaagaaaa caaaaaaagg tagtgaactt tcagctacct	3420
tttaaagagg ctaagttatc tttgataaca tcatataaag caactgttga cttcagcctg	3480
ttggtgagtt tagttgtgca tgcctttgtt gtatataaag taaattctag tgacccatgt	3540
gtcaaaaatc ttactttctac atttttttgt atttattttc tactgtgtaa atgtattcct	3600
ttgtagaatc atggttgttt tgtctcacgt gataattcag aaaatccttg ctcgttccgc	3660
aaatcctaaa gctccttttg gagatgatag aggatgtgaa atacagaaac ctcagtgaac	3720
tcaagaaata atgatcccag ccagactgag aaaatgtaag cagacagtgc cacagttagc	3780
tcatacagtg cctttgagca agttaggaaa agatgcccc actgggcaga cacagcccta	3840
tgggtcatgg tttgacaaac agagtgaag accatatttt agccccactc accctcttgg	3900
gtgcacgacc tgtacagcca aacacagcat ccaatatgaa taccatccc ctgaccgcat	3960
ccccagtagt cagattatag aatctgcacc aagatgttta gctttatacc ttggccacag	4020
agagggatga actgtcatcc agaccatgtg tcaggaaaat tgtgaacgta gatgaggtac	4080
atacactgcc gcttctcaa tccccagagc ctttaggaac aggagagtag actaggattc	4140
cttctcttaa aaaggtacat atatatggaa aaaaatcata ttgccgttct ttaaaaggca	4200
actgcatggt acattgttga ttgttatgac tggtagactc tggcccagcc agagctataa	4260
ttgtttttta aatgtgtctt gaagaatgca cagtgaacg gggagtagct attgggaaca	4320
gggaactgtc ctacactgct attgttgcta catgtatcga gccttgattg ctccagttta	4380
tatacagggc ctatcttgct tctacctac atctgcttga gcagtgcctc aagtacatcc	4440
ttattaggaa catttcaaac cccttttagt taagtctttc actaaggttc tcttgcatat	4500
atttcaagtg aatgttggat ctcagactaa ccatagtaat aatacacatt tctgtgagtg	4560
ctgacttgct tttgcaatat ttcttttctg atttatttaa tttcttcta tttatatgtt	4620
aaaatcaaaa atgttaaaat caatgaaata aatttgcagt taaga	4665

<210> 2
 <211> 1014
 <212> PRT
 <213> Homo Sapiens

<400> 2

Met	Val	Phe	Ser	Val	Arg	Gln	Cys	Gly	His	Val	Gly	Arg	Thr	Glu	Glu
1				5					10					15	

Val	Leu	Leu	Thr	Phe	Lys	Ile	Phe	Leu	Val	Ile	Ile	Cys	Leu	His	Val
			20					25					30		

Val	Leu	Val	Thr	Ser	Leu	Glu	Glu	Asp	Thr	Asp	Asn	Ser	Ser	Leu	Ser
		35					40					45			

Pro 50 Pro Ala Lys Leu 55 Ser Val Val Ser Phe 60 Ala Pro Ser Ser Asn
 Glu 65 Val Glu Thr Thr 70 Ser Leu Asn Asp Val 75 Thr Leu Ser Leu Leu Pro 80
 Ser Asn Glu Thr 85 Glu Lys Thr Lys Ile 90 Thr Ile Val Lys Thr Phe Asn 95
 Ala Ser Gly Val 100 Lys Pro Gln Arg Asn 105 Ile Cys Asn Leu 110 Ser Ser Ile
 Cys Asn Asp 115 Ser Ala Phe Phe Arg 120 Gly Glu Ile Met Phe 125 Gln Tyr Asp
 Lys Glu 130 Ser Thr Val Pro Gln 135 Asn Gln His Ile Thr 140 Asn Gly Thr Leu
 Thr 145 Gly Val Leu Ser 150 Leu Ser Glu Leu Lys Arg 155 Ser Glu Leu Asn Lys 160
 Thr Leu Gln Thr 165 Leu Ser Glu Thr Tyr Phe 170 Ile Met Cys Ala Thr Ala 175
 Glu Ala Gln 180 Ser Thr Leu Asn Cys Thr 185 Phe Thr Ile Lys Leu 190 Asn Asn
 Thr Met 195 Asn Ala Cys Ala Ala Ile 200 Ala Ala Leu Glu Arg 205 Val Lys Ile
 Arg 210 Pro Met Glu His Cys Cys 215 Cys Ser Val Arg Ile 220 Pro Cys Pro Ser
 Ser 225 Pro Glu Glu Leu Gly 230 Lys Leu Gln Cys Asp 235 Leu Gln Asp Pro Ile 240
 Val Cys Leu Ala Asp 245 His Pro Arg Gly Pro 250 Pro Phe Ser Ser Ser Gln 255
 Ser Ile Pro 260 Val Val Pro Arg Ala Thr 265 Val Leu Ser Gln Val 270 Pro Lys
 Ala Thr 275 Ser Phe Ala Glu Pro Pro 280 Asp Tyr Ser Pro Val 285 Thr His Asn
 Val 290 Pro Ser Pro Ile Gly Glu 295 Ile Gln Pro Leu Ser 300 Pro Gln Pro Ser

Ala Pro Ile Ala Ser Ser Pro Ala Ile Asp Met Pro Pro Gln Ser Glu
305 310 315 320

Thr Ile Ser Ser Pro Met Pro Gln Thr His Val Ser Gly Thr Pro Pro
325 330 335

Pro Val Lys Ala Ser Phe Ser Ser Pro Thr Val Ser Ala Pro Ala Asn
340 345 350

Val Asn Thr Thr Ser Ala Pro Pro Val Gln Thr Asp Ile Val Asn Thr
355 360 365

Ser Ser Ile Ser Asp Leu Glu Asn Gln Val Leu Gln Met Glu Lys Ala
370 375 380

Leu Ser Leu Gly Ser Leu Glu Pro Asn Leu Ala Gly Glu Met Ile Asn
385 390 395 400

Gln Val Ser Arg Leu Leu His Ser Pro Pro Asp Met Leu Ala Pro Leu
405 410 415

Ala Gln Arg Leu Leu Lys Val Val Asp Asp Ile Gly Leu Gln Leu Asn
420 425 430

Phe Ser Asn Thr Thr Ile Ser Leu Thr Ser Pro Ser Leu Ala Leu Ala
435 440 445

Val Ile Arg Val Asn Ala Ser Ser Phe Asn Thr Thr Thr Phe Val Ala
450 455 460

Gln Asp Pro Ala Asn Leu Gln Val Ser Leu Glu Thr Gln Ala Pro Glu
465 470 475 480

Asn Ser Ile Gly Thr Ile Thr Leu Pro Ser Ser Leu Met Asn Asn Leu
485 490 495

Pro Ala His Asp Met Glu Leu Ala Ser Arg Val Gln Phe Asn Phe Phe
500 505 510

Glu Thr Pro Ala Leu Phe Gln Asp Pro Ser Leu Glu Asn Leu Ser Leu
515 520 525

Ile Ser Tyr Val Ile Ser Ser Ser Val Ala Asn Leu Thr Val Arg Asn
530 535 540

Leu Thr Arg Asn Val Thr Val Thr Leu Lys His Ile Asn Pro Ser Gln
545 550 555 560

Asp Glu Leu Thr Val Arg Cys Val Phe Trp Asp Leu Gly Arg Asn Gly
565 570 575

Gly Arg Gly Gly Trp Ser Asp Asn Gly Cys Ser Val Lys Asp Arg Arg
580 585 590

Leu Asn Glu Thr Ile Cys Thr Cys Ser His Leu Thr Ser Phe Gly Val
595 600 605

Leu Leu Asp Leu Ser Arg Thr Ser Val Leu Pro Ala Gln Met Met Ala
610 615 620

Leu Thr Phe Ile Thr Tyr Ile Gly Cys Gly Leu Ser Ser Ile Phe Leu
625 630 635 640

Ser Val Thr Leu Val Thr Tyr Ile Ala Phe Glu Lys Ile Arg Arg Asp
645 650 655

Tyr Pro Ser Lys Ile Leu Ile Gln Leu Cys Ala Ala Leu Leu Leu
660 665 670

Asn Leu Val Phe Leu Leu Asp Ser Trp Ile Ala Leu Tyr Lys Met Gln
675 680 685

Gly Leu Cys Ile Ser Val Ala Val Phe Leu His Tyr Phe Leu Leu Val
690 695 700

Ser Phe Thr Trp Met Gly Leu Glu Ala Phe His Met Tyr Leu Ala Leu
705 710 715 720

Val Lys Val Phe Asn Thr Tyr Ile Arg Lys Tyr Ile Leu Lys Phe Cys
725 730 735

Ile Val Gly Trp Gly Val Pro Ala Val Val Val Thr Ile Ile Leu Thr
740 745 750

Ile Ser Pro Asp Asn Tyr Gly Leu Gly Ser Tyr Gly Lys Phe Pro Asn
755 760 765

Gly Ser Pro Asp Asp Phe Cys Trp Ile Asn Asn Asn Ala Val Phe Tyr
770 775 780

Ile Thr Val Val Gly Tyr Phe Cys Val Ile Phe Leu Leu Asn Val Ser
785 790 795 800

Met Phe Ile Val Val Leu Val Gln Leu Cys Arg Ile Lys Lys Lys Lys
805 810 815

Gln Leu Gly Ala Gln Arg Lys Thr Ser Ile Gln Asp Leu Arg Ser Ile
820 825 830

Ala Gly Leu Thr Phe Leu Leu Gly Ile Thr Trp Gly Phe Ala Phe Phe
835 840 845

Ala Trp Gly Pro Val Asn Val Thr Phe Met Tyr Leu Phe Ala Ile Phe
850 855 860

Asn Thr Leu Gln Gly Phe Phe Ile Phe Ile Phe Tyr Cys Val Ala Lys
865 870 875 880

Glu Asn Val Arg Lys Gln Trp Arg Arg Tyr Leu Cys Cys Gly Lys Leu
885 890 895

Arg Leu Ala Glu Asn Ser Asp Trp Ser Lys Thr Ala Thr Asn Gly Leu
900 905 910

Lys Lys Gln Thr Val Asn Gln Gly Val Ser Ser Ser Ser Asn Ser Leu
915 920 925

Gln Ser Ser Ser Asn Ser Thr Asn Ser Thr Thr Leu Leu Val Asn Asn
930 935 940

Asp Cys Ser Val His Ala Ser Gly Asn Gly Asn Ala Ser Thr Glu Arg
945 950 955 960

Asn Gly Val Ser Phe Ser Val Gln Asn Gly Asp Val Cys Leu His Asp
965 970 975

Phe Thr Gly Lys Gln His Met Phe Asn Glu Lys Glu Asp Ser Cys Asn
980 985 990

Gly Lys Gly Arg Met Ala Leu Arg Arg Thr Ser Lys Arg Gly Ser Leu
995 1000 1005

His Phe Ile Glu Gln Met
1010

<210> 3
<211> 339
<212> DNA
<213> Mus sp.

<400> 3
gatgtgcagc ttcaggagtc gggacctggc ctggtgaaac cttctcagtc tctgtccctc 60
acctgcactg tcaactggcta ctcaatcacc agtgattatg cctggaactg gatccggcag 120

tttccaggaa	acaaactgga	gtggctgggc	tacataagct	tcaatgataa	cactaactac	180
aacccatctc	tcaaaagtcg	aatctctatc	actcgagaca	catccaagaa	ccagttcttc	240
ctgcagttga	attctgtgac	tactgaggac	acagccacat	attactgtac	aaggagggtg	300
gactactggg	gtcaaggaac	ctcagtcacc	gtctcctca			339

<210> 4
 <211> 336
 <212> DNA
 <213> Mus sp.

<400> 4						
gatgttgga	tgacccaaac	tccactctcc	ctgcctgtca	gtcttggaga	tcaagcctcc	60
atctcttgca	gatctagtca	gagccttgta	cacagtaatg	gaaacaacta	tttacattgg	120
tatttgcaga	agccaggcca	gtctccaaag	ctcctgatct	acaaagtttc	caaccgattt	180
tctgggggtcc	cagacagggt	cagtggcagt	ggatcaggga	cagatttcac	actcaagatc	240
agcagagtgg	aggctgagga	tctgggagtt	tatttctgct	ctcaaagtac	acatgtttccg	300
tggacgttcg	gtggaggcac	caagctggaa	atcaaa			336

<210> 5
 <211> 360
 <212> DNA
 <213> Mus sp.

<400> 5						
caggttactc	tgaaagagtc	tggccctggg	atattgcagc	cctcccagac	cctcagtctg	60
acttgttctt	tctctgggtt	ttcactgagc	acttctgggtg	tgggtgtgag	ctggattcgt	120
cagccttcag	gaaaggggtc	ggagtggctg	gcacacattt	actgggatga	tgataagcgc	180
tataacccat	ccctgaagag	ccggctcaca	atctccaagg	atacctccag	aaaccaggta	240
ttcctcaaga	tcaccagtgt	ggacactgca	gatactgcca	catactactg	tgctcgaaga	300
gtattcatta	ttacggcctt	tgactactgg	ggccaaggca	ccactctcac	agtctcctca	360

<210> 6
 <211> 321
 <212> DNA
 <213> Mus sp.

<400> 6						
gatatccaga	tgacacagac	tacatcctcc	ctgtctgcct	ctctgggaga	cagagtcacc	60
atcagttgca	gggcaagtca	ggacattagc	aattacttaa	actggtatca	gcagaaacca	120
gatggaactg	ttaaactcct	gatctactac	acatcaaact	tacactcagg	agtcccatca	180
aggttcagtg	gcagtgggtc	tggagcagat	tattctctca	ccattggcaa	cctggagcaa	240
gaagatattg	ccacttactt	ttgccaacag	ggtaatacgc	ttccttggac	gttcggtgga	300
ggcaccaagc	tggaaatcaa	a				321

<210> 7
 <211> 366
 <212> DNA
 <213> Mus sp.

<400> 7
 cagggtttctc tgaaagagtc tggccctggg atattgcagc cctcccagac cctcagtctg 60
 acttgtttctt tctctgggtt ttactgagc acttctggta tgggtgtgag ctggattcgt 120
 cagccttcag gaaagggtct ggagtggctg gcacacattt actgggatga tgacaagcgc 180
 tataacccat cctgaagag ccggctcaca atctccaagg atacctccag caacctggta 240
 ttctcaaga tcaccagtgt ggacactgca gatactgcca catactactg tgctcgaagg 300
 gaagtacgac gtgattacta tgctatggac tactggggtc aaggaacctc agtcaccgtc 360
 tcctca 366

<210> 8
 <211> 324
 <212> DNA
 <213> Mus sp.

<400> 8
 agtattgtga tgaccagac tcccaaattc ctgcttgtct cagcaggaga caggattacc 60
 atagcctgca gggccagtca gagtgtgagt aatgatgtag cttggtacca acagaagcca 120
 gggcagtctc ctaaactgct gataaactat acatccaatc gctacactgg agtccttgat 180
 cgcttcactg gcagtggata tgggacggat ttcactttca ccatcagcac tgtgcaggct 240
 gaagacctgg cagtttattt ctgtcagcag gcttatagct ctccgtggac gttcgggtgga 300
 ggcaccaagc tggaaatcaa acgg 324

<210> 9
 <211> 339
 <212> DNA
 <213> Mus sp.

<400> 9
 gatgtgcagc ttcaggagtc gggacctggc ctggtgaaac cttctcagtc tctgtccctc 60
 acctgcactg tctactggcta ctcaatcacc agtgattatg cctggaactg gatccggcag 120
 tttccaggaa acaaactgga gtggatgggc tacataagct acagtgatta cactagctac 180
 aacctatctc tcaaaagtcg aatctctatc actcgagaca catccaagaa ccagttcttc 240
 ctgcagttga attctgtgac tactgaggac acagccacat attactgtgc aagaaggggtg 300
 gactactggg gtcaaggaac ctcagtcacc gtctcctca 339

<210> 10
 <211> 336
 <212> DNA

<213> Mus sp.

<400> 10
gatgttgtga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60
atctcttgca gatctagtca gagccttgta cacagtaatg gaaacaccta ttacattgg 120
tacctgcaga agccaggcca gtctccaaag ctctgatct acaaagtttc caaccgattt 180
tctgggggtcc cagacagggt cagtggcagt ggatcaggga cagatttcac actcaagatc 240
agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatgttccg 300
tggacgttcg gtggaggcac cacgctggaa atcaaa 336

<210> 11
<211> 339
<212> DNA
<213> Mus sp.

<400> 11
gatgtgcagc ttcaggagtc gggacctggc ctggtgaaac cttctcagtc tctgtccctc 60
acctgcactg tctactggcta ctcaatcacc agtgattatg cctggaactg gatccggcag 120
tttccaggaa acaaactgga gtggatgggc tacataagct tcagtgatag cactagctac 180
aaccatctc tcaaagtcg aatctctatc actcgagaca catccaagaa ccagttcttc 240
ctgcagttga attctgtgac tactgaggac acagccacat attactgtgc aagaaggggg 300
gactactggg gtcaaggaac ctcagtcacc gtctcctca 339

<210> 12
<211> 336
<212> DNA
<213> Mus sp.

<400> 12
gatgttgtga tgacccaaac tccactctcc ctgcctgtca gtcttggaga tcaagcctcc 60
atctcttgca gatctagtca gagccttgta cacagtaatg gaaacaccta ttacattgg 120
tacctgcaga agccaggcca gtctccaaag ctctgatct acaaagtttc caaccgattt 180
tctgggggtcc cagacagggt cagtggcagt ggatcaggga cagatttcac actcaagatc 240
agcagagtgg aggctgagga tctgggagtt tatttctgct ctcaaagtac acatcttccg 300
tggacgttcg gtggaggcac caagctggaa atcaaa 336

<210> 13
<211> 113
<212> PRT
<213> Mus sp.

<400> 13

Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Asp
 20 25 30
 Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
 35 40 45
 Leu Gly Tyr Ile Ser Phe Asn Asp Asn Thr Asn Tyr Asn Pro Ser Leu
 50 55 60
 Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
 65 70 75 80
 Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
 85 90 95
 Thr Arg Arg Val Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
 100 105 110

Ser

<210> 14
 <211> 112
 <212> PRT
 <213> Mus sp.

<400> 14

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
 1 5 10 15
 Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
 20 25 30
 Asn Gly Asn Asn Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
 35 40 45
 Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
 50 55 60
 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
 65 70 75 80
 Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
 85 90 95
 Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105 110

<210> 15
<211> 120
<212> PRT
<213> Mus sp.

<400> 15

Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Val Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys Gly Leu Glu
35 40 45

Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Arg Asn Gln Val
65 70 75 80

Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Arg Val Phe Ile Ile Thr Ala Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Leu Thr Val Ser Ser
115 120

<210> 16
<211> 107
<212> PRT
<213> Mus sp.

<400> 16

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Asn Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Ala Asp Tyr Ser Leu Thr Ile Gly Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 17
<211> 122
<212> PRT
<213> Mus sp.

<400> 17

Gln Val Ser Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln Pro Ser Gln
1 5 10 15

Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu Ser Thr Ser
20 25 30

Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys Gly Leu Glu
35 40 45

Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr Asn Pro Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser Asn Leu Val
65 70 75 80

Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Arg Glu Val Arg Arg Asp Tyr Tyr Ala Met Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Ser Val Thr Val Ser Ser
115 120

<210> 18
<211> 107
<212> PRT
<213> Mus sp.

<400> 18

Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
1 5 10 15

Asp Arg Ile Thr Ile Ala Cys Arg Ala Ser Gln Ser Val Ser Asn Asp
20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
35 40 45

Asn Tyr Thr Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
65 70 75 80

Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Ala Tyr Ser Ser Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 19
<211> 113
<212> PRT
<213> Mus sp.

<400> 19

Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Asp
20 25 30

Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Tyr Ile Ser Tyr Ser Asp Tyr Thr Ser Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80

Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Arg Val Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
100 105 110

Ser

<210> 20
<211> 112
<212> PRT
<213> Mus sp.

<400> 20

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
85 90 95

Thr His Val Pro Trp Thr Phe Gly Gly Gly Thr Thr Leu Glu Ile Lys
100 105 110

<210> 21

<211> 113

<212> PRT

<213> Mus sp.

<400> 21

Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
1 5 10 15

Ser Leu Ser Leu Thr Cys Thr Val Thr Gly Tyr Ser Ile Thr Ser Asp
20 25 30

Tyr Ala Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
35 40 45

Met Gly Tyr Ile Ser Phe Ser Asp Ser Thr Ser Tyr Asn Pro Ser Leu
50 55 60

Lys Ser Arg Ile Ser Ile Thr Arg Asp Thr Ser Lys Asn Gln Phe Phe
65 70 75 80

Leu Gln Leu Asn Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
85 90 95

Ala Arg Arg Gly Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser
100 105 110

Ser

<210> 22
<211> 112
<212> PRT
<213> Mus sp.

<400> 22

Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser
20 25 30

Asn Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser
85 90 95

Thr His Leu Pro Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

<210> 23
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA duplex with 3' dTdT overhang

<400> 23
cagacacggc cagugugatt

21

<210> 24
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA duplex with 3' dTdT overhang

<400> 24
ucacacgugg ccgugucggt

21

<210> 25
 <211> 21
 <212> RNA
 <213> Artificial
 <220>
 <223> siRNA duplex with 3' dTdT overhang
 <400> 25
 gcuagcgccc auucaauagtt 21

<210> 26
 <211> 21
 <212> RNA
 <213> Artificial
 <220>
 <223> siRNA duplex with 3' dTdT overhang
 <400> 26
 cuauugaaug ggcgcuagctt 21

<210> 27
 <211> 21
 <212> RNA
 <213> Artificial
 <220>
 <223> siRNA duplex with 3' dTdT overhang
 <400> 27
 gcuuacuccc uucaaacgatt 21

<210> 28
 <211> 21
 <212> RNA
 <213> Artificial
 <220>
 <223> siRNA duplex with 3' dTdT overhang
 <400> 28
 ucguuugaag ggaguaagctt 21

<210> 29
 <211> 21
 <212> RNA
 <213> Artificial
 <220>
 <223> siRNA duplex with 3' dTdT overhang
 <400> 29
 cccagagaa auaucugcatt 21

<210> 30
 <211> 21
 <212> RNA
 <213> Artificial

<220>

<223> siRNA duplex with 3' dTdT overhang

<400> 30

ugcagauauu ucucugggggtt

21